

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2004, 07:11:18 ; Search time 81 Seconds

(without alignments)
1318.700 Million cell updates/sec

Title: US-09-684-725-2

Perfect score: 1263

Sequence: 1 MEKLNASWVQKLEDPFQ.....LLPMTVISLVYLMALRVS I 242

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 1252 | 99.1 | 1248 | US-09-545-944-1 | Sequence 1, Appli |
| 2 | 680.5 | 53.9 | 1212 | US-09-170-496D-113 | Sequence 113, App |
| 3 | 680.5 | 53.9 | 1212 | US-09-170-496D-223 | Sequence 223, App |
| 4 | 677.5 | 53.6 | 1535 | US-09-668-680-12 | Sequence 12, Appl |
| 5 | 325.5 | 25.8 | 4080 | US-09-016-434-1346 | Sequence 1346, Ap |
| 6 | 281 | 22.2 | 1529 | US-08-858-876A-3 | Sequence 3, Appli |
| 7 | 281 | 22.2 | 1529 | US-09-472-880-3 | Sequence 3, Appli |
| 8 | 277 | 21.9 | 1088 | US-09-077-675A-6 | Sequence 6, Appli |
| 9 | 277 | 21.9 | 1088 | US-09-077-674-6 | Sequence 6, Appli |
| 10 | 277 | 21.9 | 1101 | US-09-016-434-1148 | Sequence 1148, Ap |
| 11 | 277 | 21.9 | 1101 | US-09-170-496D-87 | Sequence 87, Appl |
| 12 | 277 | 21.9 | 1101 | US-09-170-496D-209 | Sequence 209, App |

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|----|-------|------|------|---|--------------------|-------------------|
| 13 | 277 | 21.9 | 1122 | 3 | US-09-077-675A-9 | Sequence 9, Appli |
| 14 | 277 | 21.9 | 1122 | 4 | US-09-077-674-9 | Sequence 9, Appli |
| 15 | 274 | 21.7 | 1063 | 3 | US-09-077-675A-1 | Sequence 1, Appli |
| 16 | 274 | 21.7 | 1063 | 3 | US-09-077-674-1 | Sequence 1, Appli |
| 17 | 274 | 21.7 | 1092 | 3 | US-09-077-675A-15 | Sequence 15, Appl |
| 18 | 274 | 21.7 | 1092 | 4 | US-09-077-674-15 | Sequence 15, Appl |
| 19 | 274 | 21.7 | 3129 | 3 | US-09-077-675A-14 | Sequence 14, Appl |
| 20 | 274 | 21.7 | 3129 | 4 | US-09-077-674-14 | Sequence 14, Appl |
| 21 | 273 | 21.6 | 1029 | 3 | US-09-077-675A-4 | Sequence 4, Appli |
| 22 | 273 | 21.6 | 1029 | 4 | US-09-077-674-4 | Sequence 4, Appli |
| 23 | 270 | 21.4 | 1752 | 1 | US-07-629-1041-1 | Sequence 2, Appli |
| 24 | 269 | 21.3 | 1182 | 1 | US-07-629-1041-2 | Sequence 2, Appli |
| 25 | 264 | 20.9 | 936 | 2 | US-08-288-663A-13 | Sequence 13, Appl |
| 26 | 264 | 20.9 | 1228 | 2 | US-08-288-663A-3 | Sequence 3, Appli |
| 27 | 264 | 20.9 | 1229 | 2 | US-09-016-434-1428 | Sequence 1428, Ap |
| 28 | 259 | 20.5 | 1194 | 2 | US-08-288-663A-2 | Sequence 2, Appli |
| 29 | 258 | 20.4 | 1575 | 3 | US-08-858-876A-1 | Sequence 1, Appli |
| 30 | 258 | 20.4 | 1575 | 3 | US-09-472-880-1 | Sequence 1, Appli |
| 31 | 256.5 | 20.3 | 2160 | 3 | US-08-188-275A-1 | Sequence 1, Appli |
| 32 | 256.5 | 20.3 | 2162 | 4 | US-09-351-198-1 | Sequence 1, Appli |
| 33 | 256.5 | 20.3 | 2162 | 4 | US-09-113-426-1 | Sequence 1, Appli |
| 34 | 256.5 | 20.3 | 2162 | 4 | US-09-016-434-1379 | Sequence 1379, Ap |
| 35 | 256.5 | 20.3 | 2162 | 4 | US-09-355-709C-7 | Sequence 7, Appli |
| 36 | 256 | 20.3 | 1542 | 4 | US-09-761-962A-4 | Sequence 4, Appli |
| 37 | 255 | 20.2 | 1334 | 4 | US-09-761-962A-3 | Sequence 3, Appli |
| 38 | 255 | 20.2 | 1346 | 4 | US-09-761-962A-12 | Sequence 12, Appl |
| 39 | 255 | 20.2 | 1355 | 4 | US-09-761-962A-11 | Sequence 11, Appl |
| 40 | 255 | 20.2 | 1423 | 4 | US-09-761-962A-1 | Sequence 1, Appli |
| 41 | 255 | 20.2 | 1610 | 4 | US-09-761-962A-16 | Sequence 16, Appl |
| 42 | 255 | 20.2 | 1729 | 4 | US-09-761-962A-9 | Sequence 9, Appli |
| 43 | 255 | 20.2 | 2045 | 4 | US-09-761-962A-10 | Sequence 10, Appl |
| 44 | 253.5 | 20.1 | 1610 | 3 | US-08-889-108-7 | Sequence 7, Appli |
| 45 | 253.5 | 20.1 | 1610 | 5 | PCT-US94-10358-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1
US-09-545-944-1
; Sequence 1, Application US/09545944
; Patent No. 6461836
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: SARAU, HENRY
; APPLICANT: SHABON, USMAN
; APPLICANT: VAWTER, LISA
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
; FILE REFERENCE: GP70657-1
; CURRENT APPLICATION NUMBER: US/09/545,944
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 09/435,384
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-545-944-1

| | | | |
|------------------------|-----------|---------------|------|
| Alignment Scores: | 1,07e-136 | Length: | 1248 |
| Pred. No.: | 1250.00 | Matches: | 239 |
| Score: | 100.00% | Conservative: | 1 |
| Best local Similarity: | 99.58% | Mismatches: | 0 |
| Query Match: | 99.13% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-684-725-2 (1-242) x US-09-545-944-1 (1-1248)

| | | | | |
|--|----|-----|---|-----|
| | QY | 1 | MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnGlnLysLeuGluAspProPheGln | 20 |
| | Db | 10 | ATGGAAAACATTCAAGATCTCTCGGTATCTACCAGCAGAAACTAGAAGATCCATTCCAG | 69 |
| | QY | 21 | LysHisLeuAsnSerThrGluGluTyrlauAlaphelEuCySclyProArgargSerHis | 40 |
| | Db | 70 | AAACACCTGAACAGCACGAGGAGTATCTGCCTTCCTCTGCCGACTCTGGCGCAGCCAC | 129 |
| | QY | 41 | PhePheLeuProValSerValValTyrrValProilePheValValGlyValilleGlyAsn | 60 |
| | Db | 130 | TTCCTTCTCCCCTGCTCTGTGGTGATGTGCCAATTTTGTGTGGGGGTCAATGGCAAT | 189 |
| | QY | 61 | ValLeuValCysLeuValilleGluGlnHisGlnAlaMetLysThrProThrsenTyrr | 80 |
| | Db | 190 | GTCCTGGTGTGCTGGTGATTCTGCAGCACGAGGCTATGAAGACGCCACCAACTACTAC | 249 |
| | QY | 81 | LeuPheSerLeuAlaValSerAspieuLeuValleuLeuLeuGlyMetProleuGluVal | 100 |
| | Db | 250 | CCTCTTCAGCCTGGCGGTCTCTGACTCTCTGGTCTCTGCTCTCGAATAGCCCTGGAGTFC | 309 |
| | QY | 101 | TyrGluMetTrpArgAsnTyrrPropheLeuPheGlyProValGlyCyVstYrPheLysThr | 120 |
| | Db | 310 | TATGAGATGTGGCGCAACTACCCCTTCTTGTGGGGCCGTGGGTCTACTCTCAAGACG | 369 |
| | QY | 121 | AlaLeuPheGluThrValCysPheAlaSerileLeuSerileThrThrValSerValGlu | 140 |
| | Db | 370 | GCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCCGCTCAGCGTGGAG | 429 |
| | QY | 141 | ArgTyrrValAlaileLeuHisProPheArgAlalysLeuGlnSerThrArgArgAla | 160 |
| | Db | 430 | CGCTAGTGGCCATCTCTACACCGTTCGCGGCCAAAACTGCAGAGACACCGCGCGCGGCG | 489 |
| | QY | 161 | LeuArgileLeuGlylleValTrpClyPheSerValleuPheSerLeuProAsnthrSer | 180 |
| | Db | 490 | CTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCAACACACGAC | 549 |
| | QY | 181 | IleHisGlylleLysPheHistiTyrrPheProAsnGlySerLeuValProglySerAlaThr | 200 |
| | Db | 550 | ATCCATGGCATCAAGTTCCAATACTTTCCCCAATGGGTCCCTGTGCCAGGTTCGGCCACC | 609 |
| | QY | 201 | CysThrValilleLysProMetTrpileTyrrAsnPheilleGlnValThrSerPheLeu | 220 |
| | Db | 610 | TGTACGGTTCATCAAGCCCATGTGGATCTACAATTTTCATTCACGAGTCCACTCTCTCTTA | 669 |
| | QY | 221 | PheTyrlauLeuProMetThrValilleSerValleuTyrrTyrlauMetAlaLeuArgVal | 240 |
| | Db | 670 | TTCTACTCTCTCCCATGACTGTCACTAGTGTCTCTACTACCTTCATGGCACTCAGACTA | 729 |

RESULT 2
 US-09-170-496D-113
 ; Sequence 113, Application US/09170496D
 ; Patent No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AREN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 113
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-170-496D-113

Alignment Scores:

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|---------------------|----------|---------------|------|
| Pred. No.: | 5.38e-70 | Length: | 1212 |
| Score: | 680.50 | Matches: | 126 |
| Percent Similarity: | 74.67% | Conservative: | 42 |

Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 4 Gaps: 2

US-09-684-725-2 (1-242) x US-09-170-496D-113 (1-1212)

| | | | |
|----|-----|--|--------------|
| Qy | 17 | AspProPheGlnIysHisIeuAanSerThrGluGluTyrIleuAlaPhe--- | LeuCysGly 35 |
| Db | 37 | GACCCT-----GAGGACTTGAACCTGACTGACGAGGACACTGAGACTCAAGTACCTCGGG 90 | |
| Qy | 36 | ProArgArgSerHisPhePheLeuProValIserValValTyrValProIlePheValVal 55 | |
| Db | 91 | CCCAGCAGACAGAGCTTTCATGCCCATCTGCGCCACATACCTGCTGATCTTCGTGTTG 150 | |
| Qy | 56 | GlyValIleGlyAsnValIeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75 | |
| Db | 151 | GGCGCTGTGGGCAATGGGCTGACCTGTCTGTCTATCTGCGCCACAGGCCATGCGCAGC 210 | |
| Qy | 76 | ProThrAsnTyrTyrIeuPheSerLeuAlaValIserAspLeuIeuValLeuLeuLeuGly 95 | |
| Db | 211 | CCTACCAACTACTACCTTTCAGCCTGGCGGTGTCGGACCTGCTGGTGTGCTGTGGTGG 270 | |
| Qy | 96 | MetProIeuGlnValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115 | |
| Db | 271 | CTGGCCCTGGAGCTCTATGAGATGTGCACAACTACCCCTTCTGCTGGGGCTGTGGTGGC 330 | |
| Qy | 116 | CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135 | |
| Db | 331 | TGCTATTTCCGACGCTACTGTTTGAGATGCTCTGCCCTGAGTCTCAGTCTCAACGTCACT 390 | |
| Qy | 136 | ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155 | |
| Db | 391 | GCCCTGAGCGTGAACCGCTATGTGGCGTGTGCACCCACTCCAGGCGCAGGTCCATGGTG 450 | |
| Qy | 156 | ThrArgArgAlaLeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSer 175 | |
| Db | 451 | ACGGGGCCCATGTGCGCCAGTCTTGGGGCGCTGTGGGCTCTGGCATCTCTGCTGCC 510 | |
| Qy | 176 | LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195 | |
| Db | 511 | CTGGCCACACACGCTGCAGCGCATCGGACGTGCAGCTGCCGTGCCGGGGCCCGCATG 570 | |
| Qy | 196 | ProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPheIleGln 215 | |
| Db | 571 | CCAGACTCAGCTGTTTGATGCTGTGTCGCGCCACGGGCGCTCTACAACTGGTAGTGAG 630 | |
| Qy | 216 | ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235 | |
| Db | 631 | ACCACCGGCTGCTCTTCTTCTGCTGCCCATGTCATGAGCGGTCTCTACTGCTCTC 690 | |
| Qy | 236 | MetAlaLeuArgVal 240 | |
| Db | 691 | ATTGGGCTGGGACTG 705 | |

RESULT 3
US-09-170-496D-223
; Sequence 223, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human C
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-170-496D-223

Alignment Scores:
Pred. No.: 5,38e-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservatives: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 4 Gaps: 2

US-09-684-725-2 (1-242) x US-09-170-496D-223 (1-1212)

QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
DB 37 GACCTT-----GAGGACTTGAACCTGAGCTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
QY 36 ProArgArgSerHisPhePheLeuProValSerValTyrValProIlePheValVal 55
DB 91 CCCCAGCAGACAGAGCTGTTCATGCCATCTGTGCCACATACCTGCTGCTGCTGCTGCTG 150
QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 151 GCGCTGTGGGCAATGGGTGACCTGTCTGGTCACTCTGCGCCACAGGCCATGCGCAG 210
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
DB 211 CTTACCACTACTACTCTCTCAGCCTGGCGGTGCGACCTGCTGCTGCTGCTGCTGCTG 270
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 271 CTGCCCTGGAGCTATGAGATGTGGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 331 TGCTATTTCGACGCTACTGTTTGAGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 391 GCCTGAGGTGGAGCTATGTCGCGGTGGTGGCCACTCTCAGGCCAGGTCCATGGTG 450
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrGlyPheSerValLeuPheSer 175
DB 451 ACGGGGCCCATGTCGGCGGAGTGTGGGGCGTCTGGGGCTTGGGGCTTGGGGCTTGGGG 510
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 511 CTGCCCAACACCACTGTCAGCGCATCCGCGAGCTGCAGCTGCTGCTGCTGCTGCTGCTGCT 570
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGln 215
DB 571 CCAGACTCAGCTTTTGGATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 630
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
DB 631 ACCACGGCGTGTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
QY 236 MetAlaLeuArgVal 240
DB 691 ATTGGGCTGGGACTG 705

RESULT 4

US-09-668-680-12
Sequence 12, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xu, Chongjun

APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 12
LENGTH: 1535
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) (1338)
US-09-668-680-12

Alignment Scores:

Pred. No.: 1.7e-69 Length: 1535
Score: 677.50 Matches: 126
Percent Similarity: 74.22% Conservatives: 41
Best Local Similarity: 56.00% Mismatches: 55
Query Match: 53.64% Indels: 3
DB: 4 Gaps: 2

US-09-684-725-2 (1-242) x US-09-668-680-12 (1-1535)

QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
DB 163 GACCTT-----GAGGACTTGAACCTGAGCTGACGAGGCACTGAGACTCAAGTACCTGGGG 216
QY 36 ProArgArgSerHisPhePheLeuProValSerValTyrValProIlePheValVal 55
DB 217 CCCCAGCAGACAGAGCTGTTCATGCCATCTGTGCCACATACCTGCTGCTGCTGCTGCTG 276
QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 277 GCGCTGTGGCAATGGGCTGACCTGTCTGCTCATCTGCGCCACAGGCCATGCGCAGC 336
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
DB 337 CTTACCACTACTACTCTCTCAGCCTGGCGGTGTCGACCTGCTGCTGCTGCTGCTGCTGCTG 396
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 397 CTGCCCTGGAGCTATGAGATGTGGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 457 TGCTATTTCGACGCTACTGTTTGAGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 517 GCGCTGAGGTGGAAACGCTATGTGGCGCTGTGTCACCTGTCAGGCCAGGTCCATGGTG 576
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrGlyPheSerValLeuPheSer 175
DB 577 ACGGGGGCCCATGTGCGCGGAGTGTGGGGCGCTCTGGGGCTCTGGGGCTCTGGCTGCTGCT 636
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 637 CTGCCCAACACCACTGTCAGCGCATCCGCGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 696
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGln 215
DB 697 CCAGACTCAGCTGTTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235

Db 757 ACCACGGCTGCTTTCTTCTGCTGCCATGCGCATCATGAGCGTCTCTACCTGCTC 816
Qy 236 MetAlaLeuArgVal 240
Db 817 ATGGGCTCGACTG 831
RESULT 5
US-09-016-434-1346
; Sequence 1346, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1346:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g35020
; US-09-016-434-1346
Alignment Scores:
Pred. No.: 8,74e-28 Length: 4080
Score: 325.50 Matches: 86
Percent Similarity: 51.14% Conservative: 49
Best Local Similarity: 32.58% Mismatches: 76
Query Match: 25.77% Indels: 53
DB: 4 Gaps: 10
US-09-684-725-2 (1-242) x US-09-016-434-1346 (1-4080)
Qy 17 AspPropheGlnLysHisLeuAenSerThrGluGluTyrLeu----- 30
Db 421 GACCCCTTCAGCGGGCGGAGCGGCTGCTGGCGCGGCTTCGGC 480
Qy 31 -----AlaPheLeuCysGlyProArgSer----- 39
Db 481 AACGCTTCGGCAACGGCTCGGAGCGGCTCTGGCGGCACCCAGCAGCGTGGACGTG 540
Qy 40 -----HisPhePheLeuProValSerValValTyrValProPheValVal 55

Db 541 AACACGCACTACTCCAAAGTGTGTGACCGCGGTACTCGCGCTCTCTCGTGTG 600
Qy 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHis-----GlnAla 72
Db 601 GGCACGGTGGCAACACACGGGTGACGGGTTTCACGTCGGCGCGGAGAGCGTGCAGAGC 660
Qy 73 MetLysThrProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuVal 92
Db 661 CTGCAGACGACGGTGCATTACCACTGGCGACCTGGCGCTCTCCGACTGCTCACCTG 720
Qy 93 LeuLeuGlyMetProLeuGluValTyrGlu---MetTyrArgAsnTyrProPheLeuPhe 111
Db 721 CTGCTGGCATGCCCTGGAGCTGTACAACTCACTCTGGTGCACACCCCTGGGCTTC 780
Qy 112 GlyProValGlyCys-----TyrPheLysThrAlaLeuPheLysThrValCysPhe 128
Db 781 GGCAGCGCGGCTGCGCGGCTACTACTTC-----CTGGCGAGCGCTGCACCTAC 831
Qy 129 AlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAlaIleLeuHisPro 148
Db 832 GCCACGGCTCCTCAACGTGGCGACCTGAGTGTGGAGCGCTACTGCGCATCTGCCACCC 891
Qy 149 PheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeuGlyIleValTyr 168
Db 892 TTCAGGCCCAAGACCTCATGTCCCGAAGCGCACCAAGAGTTTCATCAGCGCATCTCG 951
Qy 169 GlyPheSerValLeuPheSerLeuPro-----AsnThrSer 180
Db 952 CTGCTCGGCCCTGCTGAGGCGCTATGCTGTTCACCATGGCGAGCAGACCGCAGC 1011
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal-----ProGlySer 198
Db 1012 GCCGACGGCCAGCAC-----GCCGGCGGCTGTGTGTGCACCCCGCACCATC 1056
Qy 199 AlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGlnValThrSer 218
Db 1057 CACACTGCCACCGTC-----AAGTGTGTATACAGGTCAACACACC 1095
Qy 219 PheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeu 238
Db 1096 TTCATGTCCTTCATATTCCTCCCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1155
Qy 239 ArgValSerIle 242
Db 1156 AAGCTGACCGTC 1167
RESULT 6
US-08-858-876A-3
; Sequence 3, Application US/08858876A
; Patent No. 6022856
; GENERAL INFORMATION:
; APPLICANT: Daniel CAPUT
; APPLICANT: Pascale CHALON
; APPLICANT: Pascual FERRARA
; APPLICANT: Vita NATALIO
; TITLE OF INVENTION: Type 2 Neurotensin Receptor
; TITLE OF INVENTION: (Int-R2)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,876A

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Db      737 CTGATGGCCCTC 748
|||||
RESULT 7
US-09-472-880-3
; Sequence 3, Application US/09472880
; Patent No. 6274333
;
GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
           Pascale CHALON
           Pascual FERRARA
           Vita NATALIO
TITLE OF INVENTION: Type 2 Neurotensin Receptor
(hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/472,880
FILING DATE: 28-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: CDS
LOCATION: 41..1288
;
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-472-880-3

Alignment Scores:
Pred. No.: 3,29e-23 Length: 1529
Score: 281.00 Matches: 72
Percent Similarity: 54.90% Conservative: 40
Best Local Similarity: 35.29% Mismatches: 78
Query Match: 22.25% Indels: 14
DB: 3 Gaps: 6

US-09-684-725-2 (1-242) x US-09-472-880-3 (1-1529)
Qy 46 SerValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCysLeu 65
   :: ::::
Db 146 ACCGGCTCTACTCGCTCATCTTCGCATTGGCACAGCGGGCAATGCGCTGCGTGAC 205
   :: ::::
Qy 66 ValIleLeuGlnHisGlnAlaMetLysThr---ProThrAsnTyrTyrLeuPheSerLeu 84
   :::::
Db 206 GTGGTGTGAAGCGCGCGCGGTGCGGCCCGCGCTGCCCTACCGCTGCTCAGCGCTG 265
   :::::
Qy 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGlu---Met 103
   :::::
Db 266 GCGTCTCAGCCCTGCTGCTACTGCTGGTCAAGCATGCCCATGGAGCTCTACAACTCGTG 325
   :::::

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QY 104 TrpArgAsnTyrProPheLeuPheGlyProValGlyCys-----TyrPheLysThr 120
Db 326 TGGTCCCACTACCCATGGGTCTTCGGCGATCTGGGCTGCGGTGATTAATCTTC----- 379
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 380 --GTGCGGAGCTGTGCGCCCTACGCCAGTGTGAGCGTTGCCAGCTTAAGCGCAGAG 436
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 437 CGTGCCTCGCTGTGCGCAGCGCTGCGCGCCCGCCCTCTCACCGCGCGCACC 496
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 497 CGCGGCTGTGTCACTGTGTGGTGTGCTCTCTGGGCTTGCCTGCCATGCGGTT 556
QY 181 IleHisGlyIleLysPheHisTyr---PheProAsnGlySerLeuValProGlySerAla 199
Db 557 ATCATGGACAGAACGACCAAGTGAAGCGGAGCGGAGCCCTGAGCCTGCCTCGCGT 616
QY 200 ThrCysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPhe 219
Db 617 GTGTGACGCTGTGTGAGCGCGCCGACACTTCAGGTCTTCATCAGGTGAATGTGTG 676
QY 220 LeuPheTyrLeuLeuProMetThrValIleSerValLeu-----TyrTyr 234
Db 677 GTGTCTTGGCTTCCCTTGGCCTGACCTCACTGTTCTTCTGAATGGCATCACTGTCAACAC 736
QY 235 LeuMetAlaLeu 238
Db 737 CTGATGCGCCTC 748

RESULT 8

US-09-077-675A-6
; Sequence 6, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

; LENGTH: 1088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-077-675A-6

Alignment Scores:

Pred. No.: 5.88e-23 Length: 1088
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 3 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-675A-6 (1-1088)

QY 45 ValSerValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCys 64
Db 123 GTCACAGCCACCTGCGTGGCACTCTTTCGTGGTGGGTATCGCTGGCACTGTCCACATG 182
QY 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 183 CTGTGTGTGTCGGCTTCCGCGAGCTGCGCACCAACCACTCTACTGTCCACATG 242
QY 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGluMetTrp 104
Db 243 GCCTTCTCCCATCTGCTCATCTTCTCTGC---ATGCCCTGGACCTCGTTCGCTCTG 299
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 300 CAGTACCGCGCTTGGAACTTCGGCGACCTCTCTGCAAACTCTTCAATTCGTCAGTGAG 359
QY 125 ThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 360 AGTGCACCTACGCCACGGTCTCACATCACAGCGCTGAGCGCTGAGCGCTACTTCGCC 419
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgArgAlaLeuArgIleLeu 164
Db 420 ATCTGCTTCCACTCCGCGGCAAGGTGGTGTGTCACCAAGGGGGGTGAGCTGGTCAATC 479
QY 165 GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 480 TTCGTATCTGGCGCGTGGCTTCTGCGAGCGCGCGGCCCATCTTCGTGCTAGTCGGGGTG 539
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 540 GAGCACGAG-----AACGCGACCGACCTTGGGACACCAACGAGTCCGCCCCOACC 590
QY 194 --LeuValProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPhe 212
Db 591 GAGTTTGGGTGGCTCTGAGCTGCTCAGGTGATG-----GTGTGGGTG----- 635
QY 213 IleIleGlnValThrSerPheLeuPheLysLeuLeuProMetThrValIleSerValLeu 232
Db 636 -----TCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 680
QY 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 681 TACAGTCTCATCGCGCAGGAAGCTG 704

RESULT 9

US-09-077-674-6
; Sequence 6, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.

APPLICANT: Van Der Ploegs, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19589P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-674-6

Alignment Scores:
Pred. No.: 5,88e-23 Length: 1088
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 4 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-674-6 (1-1088)

Qy 45 valservValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCys 64
Db 123 GTCACAGCCACCTCGCGTGGCACTCTTCGTGGTGGTATCGTGGCAACCTGCTCACCATG 182
Qy 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 183 CTGTGGTGTGGCGCTCCCGAGCTGCGCAGCACCACCACTTACCTGCTGCGCAGCATG 242
Qy 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGluMetTrrp 104
Db 243 GCCTCTCCGATCTGCTCACTTCCTCTGC-ATGCCCTGAGACCTGCTGCGCTCTGG 299
Qy 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 300 CAGTACCGGCGCTGGAACCTTCGGCGACCTCTCTGCAAACTCTTCCAATTCGTCACTGAG 359
Qy 125 ThrValCysPheAlaSerIleLeuSerIleThrValSerValGluArgTyrValAla 144
Db 360 AGCTGACCTACCGCCAGCGGTCTACCATCAGCGCTGAGCGCTGAGCGCTACTTCGCC 419
Qy 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeu 164
Db 420 ATCTGCTTCCCACTCCCGGCGCAAGGTGGTGTGTCACCAAGCGGCGGTGAGCTGGTCATC 479

Qy 165 GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 480 TTGTCATCTGGCGCGTGGCTTCTGTCAGCGCGCGGCCCATCTTCGTGCTAGTCGGGTG 539
Qy 185 LysPheHisTyrPheProAsnGlySer- 193
Db 540 GAGCAGCAG- 590
Qy 194 ---LeuValProGlySerAlaThrCysThrValIleLysProMetTrrpIleTyrAsnPhe 212
Db 591 GAGTTTGGGTGGCTCTGCGACTGCTCAGCGTCAATG- 635
Qy 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 636 -TCCAGCATCTTCTTCT 680
Qy 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 681 TACAGTCTCATCGCGCAGGAGCTG 704
RESULT 10
US-09-016-434-1148
; Sequence 1148, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1504140
US-09-016-434-1148
Alignment Scores:
Pred. No.: 5.98e-23 Length: 1101
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69

| | | | |
|--|----------|--|------|
| Query Match: | 21.93% | Indels: | 26 |
| DB: | 4 | Gaps: | 5 |
| US-09-684-725-2 (1-242) x US-09-016-434-1148 (1-1101) | | | |
| Qy | 45 | ValSerValValTyrrValProIlePheValValGlyValIleGly | |
| Db | 136 | GTACACGACCACTCGGTGGCACTCTTCGTGGTGGGTATCGCTGGG | |
| Qy | 65 | LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrr | |
| Db | 196 | CTGGTGGTTCGGCTTCGGGAGCTGGCAACCAACCAACCACTCT | |
| Qy | 85 | AlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGln | |
| Db | 256 | GCCTCTCCGATCTGCTCATCTCCTCTGC- --ATGCCCTCGAGAA | |
| Qy | 105 | ArgAsnTyrrProPheLeuPheGlyProValGlyCysTyrrPheLys | |
| Db | 313 | CAGTACCCGGCCCTCGAACTTCGGCACTCTCTGC AAACTCTCT | |
| Qy | 125 | ThrValCysPheAlaSerIleLeuSerIleThrThrValSerVal | |
| Db | 373 | AGCTGCACCTACGCCACGGTGCTCACCACTCAGAGCGCTGAGCGT | |
| Qy | 145 | IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgArg | |
| Db | 433 | ATCTGCTTCCCACTCCCGGGCCCAAGTGGTGGTCAACCAAGGGCGG | |
| Qy | 165 | GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThr | |
| Db | 493 | TTCTGCATCTGGCGCGTGGCCCTCTGCAGCGCGGGCCCATCTCT | |
| Qy | 185 | LysPheHisTyrrPheProAsnGlySer----- | |
| Db | 553 | GAGCAGCAG-----AACGGCACCGACCCCTTGGGACACCAAA | |
| Qy | 194 | ---LeuValProGlySerAlaThrCysThrValIleLysProMetMet | |
| Db | 604 | GAGTTTGGGTGGCTCTGGAGTCTCACGGTCA TG-----GTCT | |
| Qy | 213 | IleIleGlnValThrSerPheLeuPheTyrrLeuLeuProMetThr | |
| Db | 649 | -----TCCAGCATCTCTTCTCTCTCTCTCTCTCTCTCTCTCT | |
| Qy | 233 | TyrrTyrrLeuMetAlaLeuArgVal 240 | |
| Db | 694 | TACAGTCTCATCGGCAGGAAGCTG 717 | |
| RESULT 11 | | | |
| US-09-170-496D-87 | | | |
| ; Sequence 87, Application US/09170496D | | | |
| ; Patent No. 6555339 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Behan, Dominic P. | | | |
| ; APPLICANT: Chalmers, Derek T. | | | |
| ; APPLICANT: Liaw, Chen W. | | | |
| ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutive | | | |
| ; TITLE OF INVENTION: Receptors | | | |
| ; FILE REFERENCE: AREN-0040 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/170,496D | | | |
| ; CURRENT FILING DATE: 1998-10-13 | | | |
| ; NUMBER OF SEQ ID NOS: 294 | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | |
| ; SEQ ID NO 87 | | | |
| ; LENGTH: 1101 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-09-170-496D-87 | | | |
| Alignment Scores: | | | |
| Pred. No.: | 5,98e-23 | Length: | 1101 |
| Score: | 277.00 | Matches: | 66 |

[illegible]


```

Pred. No.: 5.98e-23 Length: 1101
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 4 Gaps: 5

US-09-684-725-2 (1-242) x US-09-170-496D-209 (1-1101)

QY 45 valserValValTyrValProLeuPheValValGlyValLeuValGlyAsnValLeuValCys 64
Db 136 GTACAGCACCCCTGCGTGCACCTCTCGTGGTGGTATCGCTGGCAACCTGCTACCATG 195
QY 65 LeuValLeuLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 196 CTGTGTGTGGCTTCGGAGCTTCGGCAGCTGCACACACCACTTACCTGCTGCGAGCATG 255
QY 85 AlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluValTyrGluMetTyr 104
Db 256 GCCTTCTCCGATCTGCTATCTCTCTCTGCG---ATGCCCTGGACCTGCTGCGCTCTGG 312
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 313 CAGTACCGGCGCTGGAACTTCGGCAGCTTCCTCTGCAAACTCTTCAATTCGTCACTGAG 372
QY 125 ThrValCysPheAlaSerLeuLeuSerLeuThrValSerValGluArgTyrValAla 144
Db 373 AGCTGACCTACGCCAGCTGCTCACCATCAGCGCTGAGCGCTGAGCGCTACTTCGCC 432
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgArgAlaLeuArgIleLeu 164
Db 433 ATCTGCTTCCACTTCGGGCCAGGTGGTGGTGCACCAAGGGCGGTGAGCTGTCATC 492
QY 165 GlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 493 TTGCTATCTGGCGCTGCTGCTGCGCGCGGCCCTCTCTGCTGCTGCTGCTGCTGCTG 552
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 553 GAGCAGCAG-----AACGGCAGCCAGCCCTTGGGACACCAACGAGTGGCGCCCCACC 603
QY 194 ---LeuValProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPhe 212
Db 604 GAGTTTGGGTGGCTGCTGAGCTGCTCAGCTCATG-----GTGGGGTG----- 648
QY 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 649 -----TCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 693
QY 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 694 TACAGTCTCATCGGCAGGAAGCTG 717

RESULT 13
US-09-077-675A-9
; Sequence 9, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/077,675A
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-675A-9

Alignment Scores:
Pred. No.: 6.15e-23 Length: 1122
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 3 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-675A-9 (1-1122)

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Db 388 GTACAGCACCCCTGCGTGCACCTCTCGTGGTGGTATCGCTGGCAACCTGCTACCATG 447
QY 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 448 CTGTGTGTGGCTTCGGAGCTTCGGCAGCTGCACACCACTTCTCTCTCTCTCTCTCTCT 507
QY 85 AlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluValTyrGluMetTyr 104
Db 508 GCCTTCTCCGATCTGCTATCTCTCTCTGCG---ATGCCCTGGACCTGCTGCGCTCTGG 564
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 565 CAGTACCGGCGCTGGAACTTCGGCAGCTTCCTCTGCAAACTCTTCCAAATTCGTCACTGAG 624
QY 125 ThrValCysPheAlaSerLeuLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 625 AGCTGACCTACGCCAGCTGCTCACCATCAGCGCTGAGCGCTGAGCGCTACTTCGCC 684
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgArgAlaLeuArgIleLeu 164
Db 685 ATCTGCTTCCACTTCGGGCCAGGTGGTGGTGCACCAAGGGCGGTGAGCTGTCATC 744
QY 165 GlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 745 TTGCTATCTGGCGCTGCTGCTGCGCGCGGCCCTCTCTGCTGCTGCTGCTGCTGCTG 804
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 805 GAGCAGCAG-----AACGGCAGCCAGCCCTTGGGACACCAACGAGTGGCGCCCCACC 855
QY 194 ---LeuValProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPhe 212
Db 856 GAGTTTGGGTGGCTGCTGAGCTGCTCAGCTCATG-----GTGGGGTG----- 900
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REGISTRATION NUMBER: 42,452
 REFERENCE/DOCKET NUMBER: 19590P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-594-1273
 TELEFAX: 732-594-4720
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1063 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-077-675A-1

Alignment Scores:
 Pred. No.: 1,27e-22 Length: 1063
 Score: 274.00 Matches: 66
 Percent Similarity: 54.33% Conservative: 47
 Best Local Similarity: 31.73% Mismatches: 69
 Query Match: 21.69% Indels: 26
 DB: 3 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-675A-1 (1-1063)

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Qy 45 valserValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCys 64
Db 98 GTACCGCCACCTCGCGTGGCGCTTCTGGTGGGTATCGCGGGCAACCTGCTCAGATG 157
Qy 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 158 CTGGTAGTGCAGCTTCCCGGAGATGGCGACCAACCACCACTCTACTGTCCAGCATG 217
Qy 85 AlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluValTyrGluMetTrp 104
Db 218 GCCTTCTCCGACCTACTCATCTCTCTGCG--ATGCCCTCGACCTCTTCGCGCTCTGG 274
Qy 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 275 CAGTACCGGCTTGGACCTTGGCAACCTCTCTGCAACCTCTTCCAGTTCTGTTAGCGAG 334
Qy 125 ThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 335 AGGTGACCTACCGCCACAGTGTCCATCATCCCGCTGAGCGCTGAGCGCTACTTCGCC 394
Qy 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeu 164
Db 395 ATCTGCTTCCGCTGCGGGCCAGGTAGTGTACCAAGGGCCGGTAAGCTGGTCATC 454
Qy 165 GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 455 CTGTCATCTGGCGCGGCTTCTGTCAGCGCGGCCCATCTTCGTGCTGGTCGGAGTG 514
Qy 185 LysPheHisTyrPheProAsnGlySer-----193
Db 515 GAG-----CATGATAACGGCAGTACCTCGGACACCAACAGAGTCCCGCCACG 565
Qy 194 --LeuValProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPhe 212
Db 566 GAGTTCGGCTGGCGCTCCGGCTGCTTACCGTATG-----GTCGGGGT-----610
Qy 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 611 -----TCCAGTGCTCTTCTTCTCTGCTCTCTCTGCTCTCTCTGCTCTCTGCTC 655
Qy 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 656 TATAGCCTCATCGGAGGAGCTC 679
    
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Search completed: February 16, 2004, 08:18:52
 Job time : 89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2004, 08:10:04 ; Search time 325 Seconds
(without alignment)

2742.890 Million cell updates/sec

Title: US-09-684-725-2

Perfect score: 1263

Sequence: 1 MEKLNQASWVQKLEDPFQ.....LLPMTVISVLYLMALRVS I 242

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2449703 segs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QWFASTAP -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PTC_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PTC_US_PUBCOMB.seq:
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| C | 1 | 1263 | 100.0 | 801 | 11 | US-09-782-974C-17 | Sequence 17, Appl |
| | 2 | 1252 | 99.1 | 1239 | 15 | US-10-225-567A-556 | Sequence 556, App |
| | 3 | 1252 | 99.1 | 1248 | 12 | US-10-417-820A-11 | Sequence 11, Appl |
| | 4 | 1252 | 99.1 | 1248 | 13 | US-10-272-983-11 | Sequence 11, Appl |
| | 5 | 1252 | 99.1 | 1248 | 13 | US-10-393-807-11 | Sequence 11, Appl |
| | 6 | 680.5 | 53.9 | 1212 | 13 | US-10-353-690-9 | Sequence 9, Appl |
| | 7 | 680.5 | 53.9 | 1212 | 15 | US-10-083-168-13 | Sequence 13, Appl |
| | 8 | 680.5 | 53.9 | 1212 | 15 | US-10-083-168-82 | Sequence 82, Appl |
| | 9 | 680.5 | 53.9 | 1212 | 15 | US-10-251-385-113 | Sequence 113, Appl |
| | 10 | 680.5 | 53.9 | 1212 | 15 | US-10-251-385-223 | Sequence 223, App |
| | 11 | 680.5 | 53.9 | 1212 | 15 | US-10-225-567A-539 | Sequence 539, App |
| | 12 | 680.5 | 53.9 | 1212 | 15 | US-10-290-078-16 | Sequence 16, Appl |
| | 13 | 680.5 | 53.9 | 1212 | 15 | US-10-290-078-17 | Sequence 17, Appl |
| | 14 | 677.5 | 53.6 | 1349 | 12 | US-10-240-145-96 | Sequence 96, Appl |
| | 15 | 677.5 | 53.6 | 1535 | 12 | US-10-240-145-10 | Sequence 10, Appl |
| | 16 | 677.5 | 53.6 | 1535 | 15 | US-10-146-419-12 | Sequence 12, Appl |
| | 17 | 677.5 | 53.6 | 1535 | 15 | US-10-146-419-12 | Sequence 12, Appl |
| | 18 | 418 | 33.1 | 1258 | 9 | US-09-804-551B-25 | Sequence 25, Appl |
| | 19 | 418 | 33.1 | 1287 | 15 | US-10-270-333-113 | Sequence 113, App |
| | 20 | 418 | 33.1 | 4314 | 15 | US-10-270-333-112 | Sequence 112, App |
| | 21 | 352 | 27.9 | 1788 | 15 | US-10-270-333-194 | Sequence 194, App |
| | 22 | 338 | 26.8 | 1293 | 12 | US-10-157-317-160 | Sequence 160, App |
| | 23 | 338 | 26.8 | 1293 | 12 | US-10-157-339-160 | Sequence 160, App |
| | 24 | 338 | 26.8 | 1293 | 13 | US-10-157-305A-160 | Sequence 160, App |
| | 25 | 338 | 26.8 | 1293 | 13 | US-10-157-391-160 | Sequence 160, App |
| | 26 | 338 | 26.8 | 1293 | 13 | US-10-157-096-160 | Sequence 160, App |
| | 27 | 338 | 26.8 | 1293 | 13 | US-10-157-215A-160 | Sequence 160, App |
| | 28 | 338 | 26.8 | 1293 | 13 | US-10-157-302-160 | Sequence 160, App |
| | 29 | 338 | 26.8 | 1293 | 13 | US-10-154-951B-160 | Sequence 160, App |
| | 30 | 338 | 26.8 | 1293 | 13 | US-10-157-299-160 | Sequence 160, App |
| | 31 | 338 | 26.8 | 1293 | 13 | US-10-156-831-160 | Sequence 160, App |
| | 32 | 338 | 26.8 | 1293 | 13 | US-10-156-902-160 | Sequence 160, App |
| | 33 | 338 | 26.8 | 1293 | 13 | US-10-157-147-160 | Sequence 160, App |
| | 34 | 338 | 26.8 | 1293 | 13 | US-10-157-166-160 | Sequence 160, App |
| | 35 | 338 | 26.8 | 1293 | 13 | US-10-157-318-160 | Sequence 160, App |
| | 36 | 338 | 26.8 | 1293 | 13 | US-10-156-811-160 | Sequence 160, App |
| | 37 | 338 | 26.8 | 1293 | 13 | US-10-157-320A-160 | Sequence 160, App |
| | 38 | 338 | 26.8 | 1293 | 13 | US-10-157-418A-160 | Sequence 160, App |
| | 39 | 338 | 26.8 | 1626 | 12 | US-10-157-317-162 | Sequence 162, App |
| | 40 | 338 | 26.8 | 1626 | 12 | US-10-157-339-162 | Sequence 162, App |
| | 41 | 338 | 26.8 | 1626 | 13 | US-10-157-305A-162 | Sequence 162, App |
| | 42 | 338 | 26.8 | 1626 | 13 | US-10-157-391-162 | Sequence 162, App |
| | 43 | 338 | 26.8 | 1626 | 13 | US-10-157-096-162 | Sequence 162, App |
| | 44 | 338 | 26.8 | 1626 | 13 | US-10-157-215A-162 | Sequence 162, App |
| | 45 | 338 | 26.8 | 1626 | 13 | US-10-157-302-162 | Sequence 162, App |

ALIGNMENTS

RESULT 1

US-09-782-974C-17/c
; Sequence 17, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782.974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396

; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-17

Alignment Scores:
Pred. No.: 2,58e-139 Length: 801
Score: 1263.00 Matches: 242
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-684-725-2 (1-242) x US-09-782-974C-17 (1-801)

QY 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnGlnLysLeuGluAspProPheGln 20
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QY 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuGlyCysGlyProArgGlnHis 40
DB 735 AAACACCTGAACGACCGAGGAGTATCTGGCCCTCTCTGGGACCTCGGGCGAGCCAC 676
QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
DB 675 TTCTTCTCCCGTGTCTGGGTATGTGCCAATTTTGTGGTGGGGTCTATTGGCAAT 616
QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
DB 615 GTCTGTGTGTCTGTGTATCTTCGACGACCCAGGCTATGAGACGCCACCACTACTAC 556
QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
DB 555 CTCTTCAGCCTGGCGGCTCTGACCTCTGCTCTCTCTGGAATGCCCTGGAGGTC 496
QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
DB 495 TATGAGATGTGGCGCAACTACCCCTTTCTTGTTCGGGCGGCTGGCTGCTACTTCAAGAG 436
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
DB 435 GCCTCTTTGAGACCGGTGCTTCGGCTTCATCCTCAGCATCACCACCGCTCAGCGGGAG 376
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
DB 375 CGTACTGTGGCCATCTTACACCGTTCGGCGCCAACTGCAGAGCACCGGGCGCGGCC 316
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
DB 315 CTGAGGATCTCGGATGCTGGGGCTTCTCGTGTCTCTCTCTCTCTCTCTCTCTCTCT 256
QY 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
DB 255 ATCCATGGCATCAAGTTCCTACTTCTCCCAATTTGGGTCTGGTCTGGTCTGGTCTGG 196
QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
DB 195 TGTACGGTATCAAGCCCATGTGATCTCAATTTATCATCATCAGGTACCTCTCTCTCT 136
QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240

DB 135 TTCTACCTCTCCCATGACTGTGCATCACTGTCTACTACCTCATGCACTCAGAGTG 76
QY 241 SerIle 242
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RESULT 2
US-10-225-567A-556
; Sequence 556, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 556
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-556

Alignment Scores:
Pred. No.: 9.97e-138 Length: 1239
Score: 1232.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 15 Gaps: 0

US-09-684-725-2 (1-242) x US-10-225-567A-556 (1-1239)

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DB 1 ATGGAAAACCTTCAGATGCTTCCTGGATCTACACGAGAACTAGAGATCCATCCAG 60
QY 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuGlyCysGlyProArgGlnHis 40
DB 61 AAACACCTGAACGACCGAGGAGTATCTGGCCCTCTCTGGGACCTCGGGCGAGCCAC 120
QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
DB 121 TTCTTCTCCCGTGTCTGGTGTATGTGCCAATTTTGTGGTGGGGTCTATTGGCAAT 180
QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
DB 181 GTCTGTGTGTCTGGGTGATTCGACGACCCAGGCTATGAGACGCCACCACTACTAC 240
QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
DB 241 CTCTTCAGCCTGGCGGCTCTGACCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
DB 301 TATGAGATGTGGCGCAACTACCCCTTTCTTGTTCGGGCGGCTGGGCTGCTACTTCAAGAG 360
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
DB 361 GCCTCTTTGAGACCGGTGCTTCGGCTTCATCCTCAGCATCACCACCGCTCAGCGTGGAG 420
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
DB 421 CGCTACGTGGCCATCTTACACCGGTTCCGGCGCCAACTGCAGAGCACCGGGCGCGGCC 480
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180

Db 481 CTCAGGATCTCGGCATGCTCTGGGCTTCTCCGTGCTCTCTCCCTCCCAACACCCAGC 540
QY 181 IleHisGlyLeuLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 541 ATCCATGGCATCAAGTTCACACTACTTCCCAATGGTCCCTGGTCCAGGTTCCGCCACC 600
QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleGlnValThrSerPheLeu 220
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QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
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RESULT 3

US-10-417-820A-11
; Sequence 11, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-11

Alignment Scores:
Pred. No.: 1,01e-137 Length: 1248
Score: 1252.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 12 Gaps: 0

US-09-684-725-2 (1-242) x US-10-417-820A-11 (1-1248)
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Db 10 ATGAAATACTCAGATGCTCTCGATCTACCAAGCAAACTAGAGATCCATTCCAG 69

QY 21 LysHisLeuAsnSerThrGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
Db 70 AAACACCTGAACAGACCGAGGAGTATCTGGCTTCTCTGCGGACCTCGGCGACCCAC 129
QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
Db 130 TTCTTCTCCCTGGTGTATGTGTGTATGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGT 189
QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
Db 190 GTCTGT 249
QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluVal 100
Db 250 CTCTTCAGCTCTGGGCTCTGTGACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 309
QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
Db 310 TATGAGATGTGGGCAACTACCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 369
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GCCTCTCTTTCAGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 429
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 430 CGTACGTGTGGCATCTCTACACCGCTTCCGCGCCCAAACTGCAGAGACCCCGCCG 489
QY 161 LeuArgIleLeuGlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGGATCTCGGCATCGTGTGGGCTTCTCGTGTCTCTCTCTCTCTCTCTCTCTCT 549
QY 181 IleHisGlyLeuLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCCATGGCATCAAGTTCACACTACTTCCCAATGGTCCCTGGTCCAGGTTCCGCCACC 609
QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleGlnValThrSerPheLeu 220
Db 610 TGTACGGTCATCAAGCCCATGGATCTCAATTTTCATCATCCAGGTACCTCTCTCTCT 669
QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACTCTCTCCCATGACTGTGCATGCTCTCTACTACTCTCTCTCTCTCTCTCTCT 729

RESULT 4

US-10-272-983-11
; Sequence 11, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28

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; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-11

Alignment Scores:
Pred. No.: 1,01e-137 Length: 1248
Score: 1252.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 13 Gaps: 0

US-09-684-725-2 (1-242) x US-10-272-983-11 (1-1248)

Qy 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnLysLeuGluAspProPheGln 20
Db 10 ATGGAAAACTTCAGAAATGCTTCTGGATCTACAGCAGAACTAGAGATCCATTCCAG 69
Qy 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
Db 70 AAACACCTGAACAGCCGAGGAGTATCTGGCTTCTCTGGGACCTCGGCGCAGCCAC 129
Qy 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
Db 130 TTCTTCTCCCGGTCTGTGGTGTATGTGCAATTTTCTGGTGGGGGTCAATGGCAAT 189
Qy 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
Db 190 GTCCTGGTGTGCTGTGGTGTATCTGACGACGAGCTATGAAGACGCCACCACTACTAC 249
Qy 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
Db 250 CTCCTTCAGCTCGGGGTCTCTGACCTCTCTGCTCTCTCTGCTCTCTGCTCTCTGCTCT 309
Qy 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
Db 310 TATGAGATGGGCGCACTACCTCTTCTTCTGGGCGGCGGCTGCTACTTCAAGAGC 369
Qy 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GCCTCTTTGAGACCGGTGCTTCGCTCCATCTCAGCATCACACCTCAGCGTGGAG 429
Qy 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 430 CGCTACGTGGCCATCTACACCGGTTCCGCGCCAACTGCAGAGCACCCGGCGCGGCGC 489
Qy 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGGATCTCGGCATCGCTCGGGCTTCTCGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCATGGCAATCAAGTTCCACTACTTCCCAATGGGTCTCTGCTCCAGGTTCGGCCACC 609
Qy 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
Db 610 TGTACGGTCAATCAAGCCCATGTGGATCTACAAATTTTCATCATCATCAGGTCACTCTCT 669
Qy 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACCTCTCCCATGACTGTGTCAGTGTCTCTACTACCTCACTCACTCACTCACTCA 729

RESULT 5
US-10-393-807-11

; Sequence 11, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-11

Alignment Scores:
Pred. No.: 1,01e-137 Length: 1248
Score: 1252.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 13 Gaps: 0

US-09-684-725-2 (1-242) x US-10-393-807-11 (1-1248)

Qy 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnLysLeuGluAspProPheGln 20
Db 10 ATGGAAAACTTCAGAAATGCTTCTGGATCTACAGCAGAACTAGAGATCCATTCCAG 69
Qy 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
Db 70 AAACACCTGAACAGCCGAGGAGTATCTGGCTTCTCTGGGACCTCGGCGCAGCCAC 129
Qy 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
Db 130 TTCTTCTCCCGGTCTGTGGTGTATGTGCAATTTTCTGGTGGGGGTCAATGGCAAT 189
Qy 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
Db 190 GTCCTGGTGTGCTGTGGTGTATCTGACGACGAGCTATGAAGACGCCACCACTACTAC 249
Qy 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
Db 250 CTCCTTCAGCTCGGGGTCTCTGACCTCTCTGCTCTCTCTGCTCTCTGCTCTCTGCTCT 309
Qy 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
Db 310 TATGAGATGGGCGCACTACCTCTTCTTCTGGGCGGCGGCTGCTACTTCAAGAGC 369
Qy 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GCCTCTTTGAGACCGGTGCTTCGCTCCATCTCAGCATCACACCTCAGCGTGGAG 429
Qy 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 430 CGCTACGTGGCCATCTACACCGGTTCCGCGCCAACTGCAGAGCACCCGGCGCGGCGC 489
Qy 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGGATCTCGGCATCGCTCGGGCTTCTCGGTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCATGGCAATCAAGTTCCACTACTTCCCAATGGGTCTCTGCTCCAGGTTCGGCCACC 609
Qy 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
Db 610 TGTACGGTCAATCAAGCCCATGTGGATCTACAAATTTTCATCATCATCAGGTCACTCTCT 669
Qy 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACCTCTCCCATGACTGTGTCAGTGTCTCTACTACCTCACTCACTCACTCACTCA 729

RESULT 5
US-10-393-807-11
```


APPLICANT: Maciejewski-Lenior, Dominique
APPLICANT: Leonard, James N.
APPLICANT: Ortuno, Daniel
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
FILE REFERENCE: AREN-0320
CURRENT APPLICATION NUMBER: US/10/083,168
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patent in version 3.1
SEQ ID NO 13
LENGTH: 1212
TYPE: DNA
ORGANISM: Homo sapiens
US-10-083-168-13

Alignment Scores:
Pred. No.: 3,326-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservatives: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 15 Gaps: 2

US-09-684-725-2 (1-242) x US-10-083-168-13 (1-1212)

QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
Db 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGG 90

QY 36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal 55
Db 91 CCCCAGCAGACAGAGCTGTTCATGCCCATCTGTGCCATACCTGCTGATCTTCGTGGTG 150

QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
Db 151 GCGCTGTGGCAATGGGCTGACCTGTCTGGTCATCTCTGGCCACAGCCATGGCGACG 210

QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
Db 211 CCTACCAACTACTACTCTTCAGCCTGGCGGTGGACCTGCTGCTGGTGGG 270

QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
Db 271 CTGCCCCCTGGAGCTCTATGAGATGTGGCAACTACCCCTTCCTGCTGGCGGTGGTGGC 330

QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
Db 331 TGTATTTCGACGCTACTGTTTGGATGGTCTGCTGGCTTCAGTCTCAGCTCAAGTCACT 390

QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
Db 391 GCCTGAGCGTGAACGCTATGTGGCGGTGGACCCACTCCAGGCCAGGTCCATGGTG 450

QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrPheSerValLeuPheSer 175
Db 451 ACGCGGCCCATGTGGCGGAGTGTGGGGCGCTGGGGTCTTGGCCATGCTCTGCTCC 510

QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
Db 511 CTGCCCCAACACGAGCTGCACGCGATCGCGAGTCGACGTCGCTCCGCGGCCCATG 570

QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGln 215
Db 571 CCAGACTCAGCTGTTCATGCTGTGTCGCCGCCACGGGCCCTACAAATGGTAGTGAG 630

QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrLeu 235
Db 631 ACCACCGCTGTCTTCTTCCTGCTGCCATGGCCATCATGAGGCTGCTTACCTGCTC 690

QY 236 MetAlaLeuArgVal 240
Db 236 MetAlaLeuArgVal 240

Db 691 ATTGGGCTCGGACTG 705

RESULT 8
US-10-083-168-82
Sequence 82, Application US/10083168
Publication No. US20030023069A1
GENERAL INFORMATION:
APPLICANT: Liaw, Chen W.
APPLICANT: Chalmers, Derek T.
APPLICANT: Behan, Dominic P.
APPLICANT: Maciejewski-Lenior, Dominique
APPLICANT: Leonard, James N.
APPLICANT: Ortuno, Daniel
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
FILE REFERENCE: AREN-0320
CURRENT APPLICATION NUMBER: US/10/083,168
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patent in version 3.1
SEQ ID NO 82
LENGTH: 1212
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: No. US20030023069A1el Sequence
US-10-083-168-82

Alignment Scores:
Pred. No.: 3,326-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservatives: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 15 Gaps: 2

US-09-684-725-2 (1-242) x US-10-083-168-82 (1-1212)

QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
Db 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGG 90

QY 36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal 55
Db 91 CCCCAGCAGACAGAGCTGTTCATGCCCATCTGTGCCATACCTGCTGATCTTCGTGGTG 150

QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
Db 151 GCGCTGTGGCAATGGGCTGACCTGTCTGGTCATCTCTGGCCACAGCCATGGCGACG 210

QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
Db 211 CCTACCAACTACTACTCTTCAGCCTGGCGGTGGACCTGCTGCTGGTGGG 270

QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
Db 271 CTGCCCCCTGGAGCTCTATGAGATGTGGCAACTACCCCTTCCTGCTGGCGGTGGTGGC 330

QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
Db 331 TGTATTTCGACGCTACTGTTTGGATGGTCTGCTGGCTTCAGTCTCAGCTCAAGTCACT 390

QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
Db 391 GCCTGAGCGTGAACGCTATGTGGCGGTGGACCCACTCCAGGCCAGGTCCATGGTG 450

QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrPheSerValLeuPheSer 175
Db 451 ACGCGGCCCATGTGGCGGAGTGTGGGGCGCTGGGGTCTTGGCCATGCTCTGCTCC 510

QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
Db 511 CTGCCCCAACACGAGCTGCACGCGATCGCGAGTCGACGTCGCTCCGCGGCCCATG 570


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QY 36 ProArgArgSerHisPheLeuProValSerValValTyrValProPheValVal 55
DB 91 CCCCACACACAGAGCTGTTTCATGCCCATCTGTGCCACATACCTGCTGTTCTGTTG 150
QY 56 GlyValIleGlyAsnValValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 151 GCGCTGTGGCAATGGCTGACCTGTCTGTGTCATCTGCGCCACCAAGCCATGGCAG 210
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuValLeuLeuGly 95
DB 211 CCTACCAACTACTACCTCTTCAGCTGGCCGTGTGCGACCTGCTGCTGCTGGTGGC 270
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 271 CTGCCCCCTGGAGCTCTATGAGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 331 TGTATTTCGCGACGCTATGAGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 391 GCGCTGAGCGTGAGACCTATGTGCGCGGTGTCACCCACTCCAGGCCAGGTCCATG 450
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrPheSerValLeuPheSer 175
DB 451 ACGCGGCCCATGTGCGCGAGTGTGTGGCGCGTGTGGCGTGTGGCGTGTGGCGTGT 510
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 511 CTGCCCAACACAGCTGTGACGCGTGTGCGCGCGTGTGCGCGTGTGCGCGTGTG 570
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrPheAsnPheIleLeuGln 215
DB 571 CCAGACTGAGCTGTGTCATGTGTGTCGCGCGTGTGCGCGTGTGCGCGTGTGCG 630
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
DB 631 ACCACCGCGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 690
QY 236 MetAlaLeuArgVal 240
DB 691 ATTGGCGCTGGAGCTG 705

RESULT 13
US-10-290-078-17
; Sequence 17, Application US/102900078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph A.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
; FILE REFERENCE: NFI2001-288P1(M)
; CURRENT APPLICATION NUMBER: US/10/290,078
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1212)
US-10-290-078-17

Alignment Scores:
Pred. No.: 3-32e-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservativity: 42
Best Local Similarity: 56.00% Mismatches: 54
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Query Match: 53.88% Indels: 3
DB: 15 Gaps: 2
US-09-684-725-2 (1-242) x US-10-290-078-17 (1-1212)

QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
DB 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
QY 36 ProArgArgSerHisPheLeuProValSerValValTyrValProIlePheValVal 55
DB 91 CCCCACACACAGAGCTGTTTCATGCCCATCTGTGCCACATACCTGCTGCTGCTGCTG 150
QY 56 GlyValIleGlyAsnValValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 151 GCGCTGTGGCAATGGCTGACCTGTCTGTGTCATCTGCGCCACCAAGCCATGGCAG 210
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuValLeuLeuGly 95
DB 211 CCTACCAACTACTACCTCTTCAGCTGGCCGTGTGCGACCTGCTGCTGCTGCTGCTG 270
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 271 CTGCCCCCTGGAGCTCTATGAGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 330
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 331 TGTATTTCGCGACGCTATGAGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 391 GCGCTGAGCGTGAGACCTATGTGCGCGGTGTCACCCACTCCAGGCCAGGTCCATG 450
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrPheSerValLeuPheSer 175
DB 451 ACGCGGCCCATGTGCGCGAGTGTGTGGCGCGTGTGGCGTGTGGCGTGTGGCGTGT 510
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 511 CTGCCCAACACAGCTGTGACGCGTGTGCGCGCGTGTGCGCGTGTGCGCGTGTGCG 570
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrPheAsnPheIleLeuGln 215
DB 571 CCAGACTGAGCTGTGTCATGTGTGTCGCGCGTGTGCGCGTGTGCGCGTGTGCG 630
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
DB 631 ACCACCGCGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 690
QY 236 MetAlaLeuArgVal 240
DB 691 ATTGGCGCTGGAGCTG 705

RESULT 14
US-10-240-145-96
; Sequence 96, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
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QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrPileTyrAsnPheIleIleGln 215
Db 697 CCAGACTCAGCTGTTGTCATGCTGGTCCGCCACGGGCCCTCTACAAACATGGTAGTGCAG 756

QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
Db 757 ACCACCGCGCTGCTCTTCTGCTGCCCATGGCCATCATGAGCGTGTCTACCTGCTC 816

QY 236 MetAlaLeuArgVal 240
Db 817 ATGGGCTGGGACTG 831

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Search completed: February 16, 2004, 09:20:45
Job time : 333 secs